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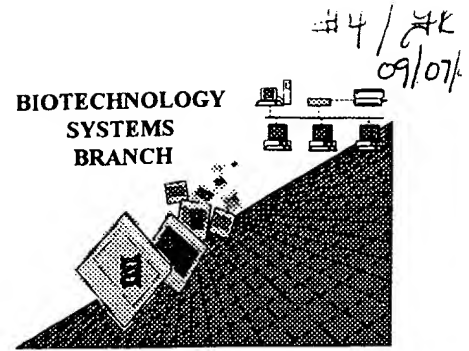Defects in the images may include (but are not limited to):

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RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: ~~09/292,436~~ 09/292,437

Art Unit / Team No. : OIPE

Date Processed by STIC: 4/28/99

GAU 1643

This paper was misfiled.

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

> **This Raw Listing contains the General Information**
> **Section and up to first 5 pages.**

Does Not Comply
Corrected Diskette Needed

```
 1    <110> APPLICANT: Olaf Schneewind
 2          Sarkis Mazmanian
 3          Gwen Liu
 4          Hung Ton-That
 5    <120> TITLE OF INVENTION: IDENTIFICATION OF SORTASE GENE
 6    <130> FILE REFERENCE: 510015.213
 7    <140> CURRENT APPLICATION NUMBER: US/09/292,436      09/292,437
 8    <141> CURRENT FILING DATE: 1999-04-15
 9    <160> NUMBER OF SEQ ID NOS: 36
10    <170> SOFTWARE: FastSEQ for Windows Version 3.0
11    <210> SEQ ID NO 1
12    <211> LENGTH: 5
13    <212> TYPE: PRT
14    <213> ORGANISM: Bacteria
15    <400> SEQUENCE: 1                    see item 10 on Err summary sheet
16          Leu Pro Xaa Thr Gly
17          1              5
18    <210> SEQ ID NO 2
19    <211> LENGTH: 621
20    <212> TYPE: DNA
21    <213> ORGANISM: Staphylococcus aureus
22    <220> FEATURE:
23    <221> NAME/KEY: CDS
24    <222> LOCATION: (1)...(621)
25    <400> SEQUENCE: 2
26          atg aaa aaa tgg aca aat cga tta atg aca atc gct ggt gtg gta ctt     48
27          Met Lys Lys Trp Thr Asn Arg Leu Met Thr Ile Ala Gly Val Val Leu
28          1               5                   10                  15
29          atc cta gtg gca gca tat ttg ttt gct aaa cca cat atc gat aat tat     96
30          Ile Leu Val Ala Ala Tyr Leu Phe Ala Lys Pro His Ile Asp Asn Tyr
31                          20                  25                  30
32          ctt cac gat aaa gat aaa gat gaa aag att gaa caa tat gat aaa aat    144
33          Leu His Asp Lys Asp Lys Asp Glu Lys Ile Glu Gln Tyr Asp Lys Asn
34                          35                  40                  45
35          gta aaa gaa cag gcg agt aaa gat aaa aag cag caa gct aaa cct caa    192
36          Val Lys Glu Gln Ala Ser Lys Asp Lys Lys Gln Gln Ala Lys Pro Gln
37                          50                  55                  60
38          att ccg aaa gat aaa tcg aaa gtg gca ggc tat att gaa att cca gat    240
39          Ile Pro Lys Asp Lys Ser Lys Val Ala Gly Tyr Ile Glu Ile Pro Asp
40          65                  70                  75                  80
41          gct gat att aaa gaa cca gta tat cca gga cca gca aca cct gaa caa    288
42          Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln
43                          85                  90                  95
44          tta aat aga ggt gta agc ttt gca gaa gaa aat gaa tca cta gat gat    336
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W--> (line 16)

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45          Leu Asn Arg Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp
46                      100                 105                 110
47          caa aat att tca att gca gga cac act ttc att gac cgt ccg aac tat        384
48          Gln Asn Ile Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr
49                      115                 120                 125
50          caa ttt aca aat ctt aaa gca gcc aaa aaa ggt agt atg gtg tac ttt        432
51          Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe
52                      130                 135                 140
53          aaa gtt ggt aat gaa aca cgt aag tat aaa atg aca agt ata aga gat        480
54          Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp
55          145                 150                 155                 160
56          gtt aag cct aca gat gta gga gtt cta gat gaa caa aaa ggt aaa gat        528
57          Val Lys Pro Thr Asp Val Gly Val Leu Asp Glu Gln Lys Gly Lys Asp
58                      165                 170                 175
59          aaa caa tta aca tta att act tgt gat gat tac aat gaa aag aca ggc        576
60          Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly
61                      180                 185                 190
62          gtt tgg gaa aaa cgt aaa atc ttt gta gct aca gaa gtc aaa taa        621
63          Val Trp Glu Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys
64                      195                 200                 205
65    <210> SEQ ID NO 3
66    <211> LENGTH: 206
67    <212> TYPE: PRT
68    <213> ORGANISM: Staphylococcus aureus
69    <400> SEQUENCE: 3
70          Met Lys Lys Trp Thr Asn Arg Leu Met Thr Ile Ala Gly Val Val Leu
71          1                   5                   10                  15
72          Ile Leu Val Ala Ala Tyr Leu Phe Ala Lys Pro His Ile Asp Asn Tyr
73                      20                  25                  30
74          Leu His Asp Lys Asp Lys Asp Glu Lys Ile Glu Gln Tyr Asp Lys Asn
75                      35                  40                  45
76          Val Lys Glu Gln Ala Ser Lys Asp Lys Lys Gln Gln Ala Lys Pro Gln
77          50                  55                  60
78          Ile Pro Lys Asp Lys Ser Lys Val Ala Gly Tyr Ile Glu Ile Pro Asp
79          65                  70                  75                  80
80          Ala Asp Ile Lys Glu Pro Val Tyr Pro Gly Pro Ala Thr Pro Glu Gln
81                      85                  90                  95
82          Leu Asn Arg Gly Val Ser Phe Ala Glu Glu Asn Glu Ser Leu Asp Asp
83                      100                 105                 110
84          Gln Asn Ile Ser Ile Ala Gly His Thr Phe Ile Asp Arg Pro Asn Tyr
85                      115                 120                 125
86          Gln Phe Thr Asn Leu Lys Ala Ala Lys Lys Gly Ser Met Val Tyr Phe
87                      130                 135                 140
88          Lys Val Gly Asn Glu Thr Arg Lys Tyr Lys Met Thr Ser Ile Arg Asp
89          145                 150                 155                 160
90          Val Lys Pro Thr Asp Val Gly Val Leu Asp Glu Gln Lys Gly Lys Asp
91                      165                 170                 175
92          Lys Gln Leu Thr Leu Ile Thr Cys Asp Asp Tyr Asn Glu Lys Thr Gly
93                      180                 185                 190
94          Val Trp Glu Lys Arg Lys Ile Phe Val Ala Thr Glu Val Lys
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 95                 195               200              205
 96    <210> SEQ ID NO 4
 97    <211> LENGTH: 227
 98    <212> TYPE: PRT
 99    <213> ORGANISM: Streptococcus pyogenes
100    <400> SEQUENCE: 4
101        Met Glu Glu Val Trp Gln Lys Ala Lys Ala Tyr Asn Ala Arg Leu Gly
102         1               5                  10                  15
103        Thr Gln Pro Val Pro Asp Ala Phe Ser Phe Arg Asp Gly Ile His Asp
104                    20                  25                  30
105        Lys Asn Tyr Glu Ser Leu Leu Gln Ile Glu Asn Asn Asp Ile Met Gly
106                35                  40                  45
107        Tyr Val Glu Val Pro Ser Ile Lys Val Thr Leu Pro Ile Tyr His Tyr
108            50                  55                  60
109        Thr Thr Asp Glu Val Leu Thr Lys Gly Ala Gly His Leu Phe Gly Ser
110        65                  70                  75                  80
111        Ala Leu Pro Val Gly Gly Asp Gly Thr His Thr Val Ile Ser Ala His
112                    85                  90                  95
113        Arg Gly Leu Pro Ser Ala Glu Met Phe Thr Asn Leu Asn Leu Val Lys
114                    100                 105                 110
115        Lys Gly Asp Thr Phe Tyr Phe Arg Val Leu Asn Lys Val Leu Ala Tyr
116                115                 120                 125
117        Lys Val Asp Gln Ile Leu Thr Val Glu Pro Asp Gln Val Thr Ser Leu
118                130                 135                 140
119        Ser Gly Val Met Gly Lys Asp Tyr Ala Thr Leu Val Thr Cys Thr Pro
120        145                 150                 155                 160
121        Tyr Gly Val Asn Thr Lys Arg Leu Leu Val Arg Gly His Arg Ile Ala
122                    165                 170                 175
123        Tyr His Tyr Lys Lys Tyr Gln Gln Ala Lys Lys Ala Met Lys Leu Val
124                180                 185                 190
125        Asp Lys Ser Arg Met Trp Ala Glu Val Val Cys Ala Ala Phe Gly Val
126                195                 200                 205
127        Val Ile Ala Ile Ile Leu Val Phe Met Tyr Ser Arg Val Ser Ala Lys
128                210                 215                 220
129        Lys Ser Lys
130        225
131    <210> SEQ ID NO 5
132    <211> LENGTH: 365
133    <212> TYPE: PRT
134    <213> ORGANISM: Actinomyces naeslundii
135    <400> SEQUENCE: 5
136        Met Gly Leu Leu Thr Tyr Pro Thr Ala Ala Ser Trp Val Ser Gln Tyr
137         1               5                  10                  15
138        Asn Gln Ser Lys Val Thr Ala Asp Tyr Ser Ala Gln Val Asp Gly Ala
139                    20                  25                  30
140        Arg Pro Asp Ala Lys Thr Gln Val Glu Gln Ala His Ala Tyr Asn Asp
141                35                  40                  45
142        Ala Leu Ser Ala Gly Ala Val Leu Glu Ala-Asn Asn His Val Pro Thr
143                50                  55                  60
144        Gly Ala Gly Ser Ser Lys Asp Ser Ser Leu Gln Tyr Ala Asn Ile Leu
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145            65                    70                    75                    80
146            Lys Ala Asn Asn Glu Gly Leu Met Ala Arg Leu Lys Ile Pro Ser Ile
147                        85                    90                    95
148            Ser Leu Asp Leu Pro Val Tyr His Gly Thr Ala Asp Asp Thr Leu Leu
149                       100                   105                   110
150            Lys Gly Leu Gly His Leu Glu Gly Thr Ser Leu Pro Val Gly Gly Glu
151                       115                   120                   125
152            Gly Thr Arg Ser Val Ile Thr Gly His Arg Gly Leu Ala Glu Ala Thr
153                       130                   135                   140
154            Met Phe Thr Asn Leu Asp Lys Val Lys Thr Gly Asp Ser Leu Ile Val
155            145                   150                   155                   160
156            Glu Val Phe Gly Glu Val Leu Thr Tyr Arg Val Thr Ser Thr Lys Val
157                       165                   170                   175
158            Val Glu Pro Glu Glu Thr Glu Ala Leu Arg Val Glu Glu Gly Lys Asp
159                       180                   185                   190
160            Leu Leu Thr Leu Val Thr Cys Thr Pro Leu Gly Ile Asn Thr His Arg
161                       195                   200                   205
162            Ile Leu Leu Thr Gly Glu Arg Ile Tyr Pro Thr Pro Ala Lys Asp Leu
163                       210                   215                   220
164            Ala Ala Ala Gly Lys Arg Pro Asp Val Pro His Phe Pro Trp Trp Ala
165            225                   230                   235                   240
166            Val Gly Leu Ala Ala Gly Leu Ile Val Val Gly Leu Tyr Leu Trp Arg
167                       245                   250                   255
168            Ser Gly Tyr Ala Ala Ala Arg Ala Lys Glu Arg Ala Leu Ala Arg Ala
169                       260                   265                   270
170            Arg Ala Ala Gln Glu Glu Pro Gln Pro Gln Thr Trp Ala Glu Gln Met
171                       275                   280                   285
172            Arg Ile Trp Met Asp Asp Asp Ala Gly Val Glu Pro Gln Arg Trp Phe
173                       290                   295                   300
174            Thr Asp Leu Pro Val Pro Pro Gln Pro Ser Glu Met Glu Asn Leu Ala
175            305                   310                   315                   320
176            Leu Leu Glu Glu Ile Ala Ser Leu Ser Ala Pro Ser Gly Arg Trp Asp
177                       325                   330                   335
178            Asp Gln Glu Leu Ile Asp Thr Ala Glu Ile Pro Val Leu Asp Ala Thr
179                       340                   345                   350
180            Arg Pro Ser Ala Gly Thr Ser Gly Arg Thr His Arg Leu
181                       355                   360                   365
182  <210> SEQ ID NO 6
183  <211> LENGTH: 284
184  <212> TYPE: PRT
185  <213> ORGANISM: Enterococcus faecalis
186  <400> SEQUENCE: 6
187            Met Lys Ser Lys Lys Lys Arg Arg Ile Ile Asp Gly Phe Met Ile Leu
188            1                     5                     10                    15
189            Leu Leu Ile Ile Gly Ile Gly Ala Phe Ala Tyr Pro Phe Val Ser Asp
190                        20                    25                    30
191            Ala Leu Asn Asn Tyr Leu Asp Gln Gln Ile Ile Ala His Tyr Gln Ala
192                        35                    40                    45
193            Lys Ala Ser Gln Glu Asn Thr Lys Glu Met Ala Glu Leu Gln Glu Lys
194            50                    55                    60
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195          Met Glu Lys Lys Asn Gln Glu Leu Ala Lys Lys Gly Ser Asn Pro Gly
196          65                  70                  75                  80
197          Leu Asp Pro Phe Ser Glu Thr Gln Lys Thr Thr Lys Lys Pro Asp Lys
198                          85                  90                  95
199          Ser Tyr Phe Glu Ser His Thr Ile Gly Val Leu Thr Ile Pro Lys Ile
200                          100                 105                 110
201          Asn Val Arg Leu Pro Ile Phe Asp Lys Thr Asn Ala Leu Leu Leu Glu
202                      115                 120                 125
203          Lys Gly Ser Ser Leu Leu Glu Gly Thr Ser Tyr Pro Thr Gly Gly Thr
204                  130                 135                 140
205          Asn Thr His Ala Val Ile Ser Gly His Arg Gly Leu Pro Gln Ala Lys
206              145                 150                 155                 160
207          Leu Phe Thr Asp Leu Pro Glu Leu Lys Lys Gly Asp Glu Phe Tyr Ile
208                          165                 170                 175
209          Glu Val Asn Gly Lys Thr Leu Ala Tyr Gln Val Asp Gln Ile Lys Thr
210                          180                 185                 190
211          Val Glu Pro Thr Asp Thr Lys Asp Leu His Ile Glu Ser Gly Gln Asp
212                      195                 200                 205
213          Leu Val Thr Leu Leu Thr Cys Thr Pro Tyr Met Ile Asn Ser His Arg
214              210                 215                 220
215          Leu Leu Val Arg Gly His Arg Ile Pro Tyr Gln Pro Glu Lys Ala Ala
216          225                 230                 235                 240
217          Ala Gly Met Lys Lys Val Ala Gln Gln Gln Asn Leu Leu Leu Trp Thr
218                      245                 250                 255
219          Leu Leu Leu Ile Ala Cys Ala Leu Ile Ile Ser Gly Phe Ile Ile Trp
220                      260                 265                 270
221          Tyr Lys Arg Arg Lys Lys Thr Thr Arg Lys Pro Lys
222                  275                 280
223   <210> SEQ ID NO 7
224   <211> LENGTH: 246
225   <212> TYPE: PRT
226   <213> ORGANISM: Streptococcus mutans
227   <400> SEQUENCE: 7
228          Met Lys Lys Glu Arg Gln Ser Arg Lys Lys Arg Ser Phe Leu Arg Thr
229          1                   5                   10                  15
230          Phe Leu Pro Ile Leu Leu Leu Val Ile Gly Leu Ala Leu Ile Phe Asn
231                          20                  25                  30
232          Thr Pro Ile Arg Asn Ala Leu Ile Ala Trp Asn Thr Asn Arg Tyr Gln
233                      35                  40                  45
234          Val Ser Asn Val Ser Lys Lys Asp Ile Glu His Asn Lys Ala Ala His
235              50                  55                  60
236          Ser Ser Phe Asp Phe Lys Lys Val Glu Ser Ile Ser Thr Gln Ser Val
237          65                  70                  75                  80
238          Leu Ala Ala Gln Met Ala Ala Gln Lys Leu Pro Val Ile Gly Gly Ile
239                          85                  90                  95
240          Ala Ile Pro Asp Leu Lys Ile Asn Leu Pro Ile Phe Lys Gly Leu Asp
241                          100                 105                 110
242          Asn Val Gly Leu Thr Tyr Gly Ala Gly Thr Met Lys Asn Asp Gln Val
243                      115                 120                 125
244          Met Gly Glu Asn Asn Tyr Ala Leu Ala Ser His His Val Phe Gly Met
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VERIFICATION SUMMARY
PATENT APPLICATION **US/09/292,436**

Input Set: **I292436.RAW**

Line	?	Error/Warning	Original Text
16	W	"N" or "Xaa" used: Feature required	Leu Pro Xaa Thr Gly
63	W	Line data has been corrected	Val Trp Glu Lys Arg Lys Ile Phe Val Ala T

CORRECTION SUMMARY
PATENT APPLICATION **US/09/292,436**

Input Set: **I292436.RAW**

Line	Original Text	Corrected Data
63	Val Trp Glu Lys Arg Lys Ile Phe Val Ala T	Val Trp.Glu Lys Arg Lys Ile Phe Val Ala T

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/292,43X

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleic
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ Wrong Designation
Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.